

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 16:54:45 ; Search time 0.001 Seconds
(without alignments)
2.040 Million cell updates/sec

Title: us-10-825-908a-1

Perfect score: 17

Sequence: 1 aatcaaaagcgatgcg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 60 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : us-10-825-908a-19:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	100.0	60	1	us-10-825-908a-19	
2	5	29.4	60	1	us-10-825-908a-19	

ALIGNMENTS

RESULT 1
us-10-825-908a-19

Query Match 100.0%; Score 17; DB 1; Length 60;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AATCAAAAGCGAATGCG 41
|||||
DB 1 AATCAAAAGCGAATGCG 17

RESULT 2
us-10-825-908a-19/c

Query Match 29.4%; Score 5; DB 1; Length 60;

Best Local Similarity 61.5%; Pred. No. 0;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 29 AAAAGCGAATGCG 41
|||
DB 22 ACATACGCATTCG 10

Search completed: August 16, 2006, 16:54:45
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 16:52:13 ; Search time 0.001 Seconds
(without alignments)
1.972 Million cell updates/sec

Title: us-10-825-908a-1
Perfect score: 17
Sequence: 1 aatcaaaagcgaatgcg 17

Scoring table: IDENTITY NJC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 58 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-10-825-908a-9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17	100.0	58 1	us-10-825-908a-9
2	5	29.4	58 1	us-10-825-908a-9

ALIGNMENTS

RESULT 1
us-10-825-908a-9

Query Match 100.0%; Score 17; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AATCAAAAGCGAATGCG 41
|||
Db 1 AATCAAAAGCGAATGCG 17

RESULT 2
us-10-825-908a-9/c

Query Match 29.4%; Score 5; DB 1; Length 58;
Best Local Similarity 61.5%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 29 AAAAGCGAATGCG 41
|
Db 22 ACATAGCGAATGCG 10

Search completed: August 16, 2006, 16:52:13
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 12:22:56 ; Search time 0.001 Seconds
(without alignments)
2.040 Million cell updates/sec

Title: us-10-825-908a-2

Perfect score: 17

Sequence: 1 actctctcatctttgc 17

Scoring table: IDENTITY NJC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 60 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : us-10-825-908a-19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16	94.1	60	1	us-10-825-908a-19
2	3.4	20.0	60	1	us-10-825-908a-19

ALIGNMENTS

RESULT 1
us-10-825-908a-19/c

Query Match 94.1%; Score 16; DB 1; Length 60;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTTCTTCATCTTTTGC 41
|||
60 CTTCTTCATCTTTTGC 45

RESULT 2
us-10-825-908a-19

Query Match 20.0%; Score 3.4; DB 1; Length 60;

Best Local Similarity 80.0%; Pred. No. 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CATCT 36
|||
Db 29 CACT 33

Search completed: August 17, 2006, 12:22:56
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 12:24:55 ; Search time 0.001 Seconds
(without alignments)
1.972 Million cell updates/sec

Title: us-10-825-908a-2
Perfect score: 17
Sequence: 1 actctcaccatttgc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 58 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-10-825-908a-9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16	94.1	58	1	us-10-825-908a-9
2	3.4	20.0	58	1	us-10-825-908a-9

ALIGNMENTS

RESULT 1
us-10-825-908a-9/c

Query Match 94.1%; Score 16; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCTCTCATCTTTTGC 41
58 CTCTCTCATCTTTTGC 43

RESULT 2
us-10-825-908a-9

Query Match 20.0%; Score 3.4; DB 1; Length 58;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CATCT 36
29 CAACT 33

Search completed: August 17, 2006, 12:24:55
Job time : 0.001 secs

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Search completed: August 18, 2006, 16:25:46
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:25:46 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-1

Perfect score: 17
Sequence: 1 aatcaaaagcgatgcg 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 4899.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	960	1	PAN908-4899
2	8	47.1	960	1	PAN908-4899

ALIGNMENTS

RESULT 1
PAN908-4899
; Entered [mrnhl 18-Aug-06 14:48]
PAN908-4899

Query Match 100.0%; Score 17; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AATCAAAAGCGAATGCG 41
|||||
DB 414 AATCAAAAGCGAATGCG 430

RESULT 2
PAN908-4899/C
; Entered [mrnhl 18-Aug-06 14:48]
PAN908-4899

Query Match 47.1%; Score 8; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCGAATGC 40
|||||
DB 686 GCGAATGC 679

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Search completed: August 18, 2006, 16:26:55
Job time : 1 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:26:54 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-1
Perfect score: 17
Sequence: 1 aatcaaaagcgaatgcg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 5929.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	960	1	PAN908-5929
2	8	47.1	960	1	PAN908-5929

ALIGNMENTS

RESULT 1
PAN908-5929
; Entered [mrhl 18-Aug-06 14:46]
PAN908-5929

Query Match 100.0%; Score 17; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AATCAAAAGCGAATGCG 41
DB 414 AATCAAAAGCGAATGCG 430

RESULT 2
PAN908-5929/C
; Entered [mrhl 18-Aug-06 14:46]
PAN908-5929

Query Match 47.1%; Score 8; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCGAATGC 40
DB 686 GCGAATGC 679

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Search completed: August 18, 2006, 15:58:35
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:58:35 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-1
Perfect score: 17
Sequence: 1 aatcaaaagcgatgcg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 6495.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	960	1	PAN908-6495
2	8	47.1	960	1	PAN908-6495

ALIGNMENTS

RESULT 1
PAN908-6495
; Entered [mrhl 18-Aug-06 15:00]
PAN908-6495

Query Match 100.0%; Score 17; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AATCAAAAGCGAATGCG 41
DB 414 AATCAAAAGCGAATGCG 430

RESULT 2
PAN908-6495/c
; Entered [mrhl 18-Aug-06 15:00]
PAN908-6495

Query Match 47.1%; Score 8; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCGAATGC 40
DB 686 GCGAATGC 679

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Search completed: August 18, 2006, 16:03:52
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:03:52 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-1

Perfect score: 17

Sequence: 1 aatcaaaagcgatgcg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 7985.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	960	1	PAN908-7985
2	8	47.1	960	1	PAN908-7985

ALIGNMENTS

RESULT 1
PAN908-7985
; Entered [mrhl 18-Aug-06 14:39]
PAN908-7985

Query Match 100.0%; Score 17; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AATCAAAAGCGAATGCG 41
|||||
DB 414 AATCAAAAGCGAATGCG 430

RESULT 2
PAN908-7985/c
; Entered [mrhl 18-Aug-06 14:39]
PAN908-7985

Query Match 47.1%; Score 8; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCGAATGC 40
|||||
DB 686 GCGAATGC 679

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Search completed: August 18, 2006, 16:29:16
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:29:16 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-2

Perfect score: 17

Sequence: 1 acctcttcaccttgc 17

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 4899.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16	94.1	960	1	PAN908-4899
2	8.4	49.4	960	1	PAN908-4899
					Entered [mrhl 18 Entered [mrhl 18

ALIGNMENTS

RESULT 1
PAN908-4899/c
; Entered [mrhl 18-Aug-06 14:48]
PAN908-4899

Query Match 94.1%; Score 16; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTTCTTCATCTTTGC 41
Db 472 CTTCTTCATCTTTGC 457

RESULT 2
PAN908-4899
; Entered [mrhl 18-Aug-06 14:48]
PAN908-4899

Query Match 49.4%; Score 8.4; DB 1; Length 960;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TTCTTCATCT 36
Db 632 TTCTTCATCT 641

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:17:06 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-2

Perfect score: 17
Sequence: 1 actcttcacatttcgc 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1 seqs, 960 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : 5929.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16	94.1	960	1	PAN908-5929 Entered [mrnhl 18
2	8.4	49.4	960	1	PAN908-5929 Entered [mrnhl 18

ALIGNMENTS

RESULT 1
PAN908-5929/c
; Entered [mrnhl 18-Aug-06 14:46]
PAN908-5929

Query Match 94.1%; Score 16; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTTCTTCATCTTTTGC 41
|||||
Db 472 CTTCTTCATCTTTTGC 457

RESULT 2
PAN908-5929
; Entered [mrnhl 18-Aug-06 14:46]
PAN908-5929

Query Match 49.4%; Score 8.4; DB 1; Length 960;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TTCTTCATCT 36
|||||
Db 632 TTCATCATCT 641

Search completed: August 18, 2006, 16:17:07
Job time : 1 secs

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Search completed: August 18, 2006, 16:30:39
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:30:39 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-2

Perfect score: 17

Sequence: 1 actctctcattctgc 17

Scoring table: IDENTITY NJC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 6495.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16	94.1	960	1	PAN908-6495
2	8.4	49.4	960	1	PAN908-6495
					Entered [mrhl 18
					Entered [mrhl 18

ALIGNMENTS

RESULT 1
PAN908-6495/c
Entered [mrhl 18-Aug-06 15:00]
PAN908-6495

Query Match 94.1%; Score 16; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCTTCATCTTGC 41
DB 472 CTCTTCATCTTGC 457

RESULT 2
PAN908-6495
Entered [mrhl 18-Aug-06 15:00]
PAN908-6495

Query Match 49.4%; Score 8.4; DB 1; Length 960;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TTCTTCATCT 36
DB 632 TTCTTCATCT 641

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Search completed: August 18, 2006, 16:31:23
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 16:31:23 ; Search time 0.001 Seconds
(without alignments)
32.640 Million cell updates/sec

Title: us-10-825-908a-2
Perfect score: 17
Sequence: 1 actcttcacatcttgc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 960 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 7985.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	16	94.1	960	1	PAN908-7985 Entered [mrhl 18
2	8.4	49.4	960	1	PAN908-7985 Entered [mrhl 18

ALIGNMENTS

RESULT 1
PAN908-7985/c
; Entered [mrhl 18-Aug-06 14:39]
PAN908-7985

Query Match 94.1%; Score 16; DB 1; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCTTCATCTTTGC 41
|||||
Db 472 CTCTTCATCTTTGC 457

RESULT 2
PAN908-7985
; Entered [mrhl 18-Aug-06 14:39]
PAN908-7985

Query Match 49.4%; Score 8.4; DB 1; Length 960;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TTCTTCATCT 36
|||||
Db 632 TTCATCATCT 641